



EX-92D

OIPE

RAW SEQUENCE LISTING

DATE: 03/11/2002

PATENT APPLICATION: US/10/081,051

TIME: 10:44:44

Input Set : A:\EP.txt

Output Set: N:\CRF3\03112002\J081051.raw

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3 <110> APPLICANT: Barbet, Anthony F.
4      Whitmire, William M.
5      Kamper, Sondra M.
6      Simbi, Bigboy H.
7      Ganta, Roman R.
8      Moreland, Annie L.
9      Mwangi, Duncan M.
10     McGuire, Travis C.
11     Mahan, Suman M.
13 <120> TITLE OF INVENTION: Ehrlichia Ruminantium Polypeptides, Antigens,
Polynucleotides, and
14     Methods of Use
16 <130> FILE REFERENCE: UF-299XC1
C--> 18 <140> CURRENT APPLICATION NUMBER: US/10/081,051
C--> 18 <141> CURRENT FILING DATE: 2002-02-20
18 <150> PRIOR APPLICATION NUMBER: US 60/269,944
19 <151> PRIOR FILING DATE: 2001-02-20
21 <160> NUMBER OF SEQ ID NOS: 117
23 <170> SOFTWARE: PatentIn version 3.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 278
27 <212> TYPE: PRT
28 <213> ORGANISM: Ehrlichia chaffeensis
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37          20          25          30
40 Ile Ser Gly Asn Phe Tyr Val Ser Gly Lys Tyr Met Pro Ser Ala Ser
41          35          40          45
44 His Phe Gly Met Phe Ser Ala Lys Glu Glu Lys Asn Pro Thr Val Ala
45          50          55          60
48 Leu Tyr Gly Leu Lys Gln Asp Trp Glu Gly Ile Ser Ser Ser Ser His
49 65          70          75          80
52 Asn Asp Asn His Phe Asn Asn Lys Gly Tyr Ser Phe Lys Tyr Glu Asn
53          85          90          95
56 Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Met Gly Gly
57          100         105         110
60 Pro Arg Val Glu Phe Glu Val Ser Tyr Glu Thr Phe Asp Val Lys Asn
61          115         120         125
64 Gln Gly Asn Asn Tyr Lys Asn Asp Ala His Arg Tyr Cys Ala Leu Gly
65          130         135         140
68 Gln Gln Asp Asn Ser Gly Ile Pro Lys Thr Ser Lys Tyr Val Leu Leu
69 145         150         155         160

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72 Lys Ser Glu Gly Leu Leu Asp Ile Ser Phe Met Leu Asn Ala Cys Tyr
73          165          170          175
76 Asp Ile Ile Asn Glu Ser Ile Pro Leu Ser Pro Tyr Ile Cys Ala Gly
77          180          185          190
80 Val Gly Thr Asp Leu Ile Ser Met Phe Glu Ala Thr Asn Pro Lys Ile
81          195          200          205
84 Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Asn Pro Glu Ala
85          210          215          220
88 Ser Val Phe Ile Gly Gly His Phe His Lys Val Ile Gly Asn Glu Phe
89 225          230          235          240
92 Arg Asp Ile Pro Thr Leu Lys Ala Phe Val Thr Ser Ser Ala Thr Pro
93          245          250          255
96 Asp Leu Ala Ile Val Thr Leu Ser Val Cys His Phe Gly Ile Glu Leu
97          260          265          270
100 Gly Gly Arg Phe Asn Phe
101          275
104 <210> SEQ ID NO: 2
105 <211> LENGTH: 4360
106 <212> TYPE: DNA
107 <213> ORGANISM: Ehrlichia ruminantium (formerly Cowdria ruminantium)
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112 tgggtggtttc gctatatctt gtaaatcaat atctaattgca tctgataata tgaattcata      120
114 ttacacttga aattctttta taattttatc atgtattggt aataatctac tgtctttctc      180
116 tatagatatt aatttttttag gattcttttt gagtattgaa taagtcattg taccaagtc      240
118 gggaccaatt tcaataattg aaaaattgct aatgtttcct gcataattaa ctattttatc      300
120 tgtaatatca gttgagttaa tgaaacattg gcttaactct tttttaggat ttatcatgta      360
122 attacttcca ataatttttt aaattggatt attaaatttt gtaaatctct aatatcatta      420
124 tactggtaag tagtatgctt atatatacaa attataattt atcagagtat tgacttttgt      480
126 gatatgtgta tataaaatac ggaaatgtta tagccgactt agcttcaatt ggtagagcaa      540
128 ctgacttgta atcagtaggt tataagttcg agtcttatag tcggcacatc attttacttt      600
130 aagtagtttt atgtcattac tcacgtttgc taactggaag atgcatgggtg atttttttac      660
132 tttttcttcg ttacaaaagg agcttagtaa ccgtttaatt aatatagaag ataaagtaaa      720
134 ggtagtatta tgcccaccat ttattgcgtt atctacttat gtttaattgtc cacataatat      780
136 taagtttggt ggacagaact gttgttatgt atctagtggg aagtacactg gagaaattag      840
138 tgctagtatg ttatataact ctggatgtag ttatgtaata gtgggtcact ctgaaaggag      900
140 gagtacgttt catgaaactg atcatgatgt taggttaaaa gctgaatgtg cgatcgaatc      960
142 aggattaata ccaattattt gtgttgga gaactttacta gatagggaaa atggtatgct      1020
144 aaaagatact ttattaagtc aatgtagtga atcttttctt aaaaatggta agtttatcat      1080
146 agcatatgag ccagtatggg caataggga caataaaaata ccttctactg atgtaataat      1140
148 agaagcttta gagattatta ggtcatatga ttatgtatct gatatacat atggtggagc      1200
150 agtaaatcat actaatgtag gtgatattgt aagtatcaat caattgtctg gtgttttagt      1260
152 tggtagtgct agtttagata tggagagttt ttttaatata atatgtagtg ctataaatgt      1320
154 gaggcaaagt taatgaagaa aatattggtt acgttttttag ttgttgtaa tgtgttttgt      1380
156 aatgctgcc aattgttcaac tgactcatca gaagataaac agtatatttt aattggtact      1440
158 ggttctatga ctggagtata ttatctata ggaggtagca tatgtagggt tattgcatct      1500
160 gattatggta atgataataa cagcatagtt tgttctatat cttctacaac tggtagcgta      1560
162 tataatctta attctatgag ttatgcaaat atggatatag gtattattca atctgattta      1620
164 gagtactatg catataatgg tattggttta tatgaaaaaa tgccagcaat gaggcatcta      1680

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166 agaataattat cttcattaca taaagaatat cttacaattg ttgttagggc gaattctaata 1740
168 atatcagtta ttgatgatata aaaaggcaaaa agagttaata ttggtagtcc tggtagtggt 1800
170 gtaagaatag caatgttaaaa attgttaaat gaaaaaggat ggggaagaaa agattttgct 1860
172 gttatggcag aattaaaaatc atcagagcaa gctcaagcat tatgtgataa taaaattgat 1920
174 gtgatggtag atgttgttgg acatcctaata gctgcaattc aagaagcagc agcaacttgt 1980
176 gatataaaat ttattttcttt agatgatgat ctcatagata aattacatac taagtatccc 2040
178 tattataaaa gggatattat tagtgggtgcg ttatacagta acttacctga tatacaaaact 2100
180 gtttcagtaa aagcttcttt aataacaact actgaattaa gcaatgagtt ggccataaaa 2160
182 gttgttaaat ctttggttag ccattttacat gaactacatg gaattactgg agctcttaga 2220
184 aatcttactg taaaagacat ggtacagtca gatattacac ctttacctga cgggtgcaaaa 2280
186 cgttattata aggaaatttg agttataaaa taaaatattg ttgtaagcaa tttgtcaaaa 2340
188 gtagtattag caatagagac aagctgtgat gaaacagctg ttgctgtcgt aagaagtgat 2400
190 aagcaagttt tatcacataa ggtacttttc caaaaaagac atgtagtcta tgggtggggt 2460
192 gtacctgaaa ttgcttctcg tgcacataat aactatttat atgacttaac ctctcaatct 2520
194 attgaggaat caggatgtga tttagcagat attgatgcta tagcagttac ttcaggtcca 2580
196 ggtcttattg gaggactaat tataggtgta atgatggcta aagctatttc cagcgttact 2640
198 aataagccta ttattgaggt taatcatctg gaagcacata ctttgcataa acgaatgttt 2700
200 catgatattg attttccatt tttagtattg atcatactcg gcggacattg tcagttttta 2760
202 atagttcatg atgttggatg ttatcaaaga ttaggttctt ctttagatga ctcccttggt 2820
204 gaagtatttg ataaagtagc aagaatgttg aatttgggat atcctggagg gccattatt 2880
206 gaaaaaaaat ccataatggg tgatagcaaa agtttttttc taccacgtgc attaatcaat 2940
208 cgtcttggtg gtgatttttc tttctccggg attaagacgg cagtaagaaa tattgttgta 3000
210 aatcaaaaat atatagataa tgattttata tgtaatatatt cagcttcttt tcaagattgt 3060
212 attggtgata tattagtaaa caggattact aatgctattc atatgtcaca agctataaat 3120
214 tgtaagatta ataagttagt agtaactgga ggtgttgcag ctaatcacct attacgtaat 3180
216 cgtatatcaa tttgtgtaaa agataataat tttgaggtgc tatatccctc aactgagtta 3240
218 tgtactgata atggaattat ggttgggtgg gctggtattg aaaatttate taaaggttat 3300
220 gtttctaata tagattttgt tccaaaagca agatggccgt tagaaagcat aaaaaggctc 3360
222 agttaattat taatacagta gtattttact atacacgatt cctattgtat atatttataa 3420
224 tattgattgg ctattataaa tttttttatt tattaaagta ctcatttttt gcaggaaaaa 3480
226 tgtttaatca gtatcaagat aatcaagcta acgacaatat ttcttattca ggtggaataa 3540
228 gaagattttc cagcactact atagagttag tatttttaat gtttgtttta caaattaata 3600
230 gtggtatttt gaaagtaaaa tagcatattc atatactaag ttattaatta actagattat 3660
232 tatgattggt gatatatgta tgcgtatatt taaaaggtta aatatactga tactactaat 3720
234 tgatagattg tgtgtatata agaaaaaaa aaagatggaa ttgttcccta atatatattat 3780
236 gtctaagtag aaatagtgtg taaagttgca atataattgg tatttatttc tagataaaat 3840
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240 tattaatagt aaaaaggat ataatatggt ttgtaagtta taatgtaata tcgtgataag 3960
242 attatgtttt tttgtgtgat tttataaata acaaattgaa cagtatataa ataccacttt 4020
244 tccttaagta attactactg ctaaaataaaa tcgtagcctt ttatatgact cttttttact 4080
246 atagaaaatt caccaatcta acaatagtaa ataaaaattt ttaattttat atgacatttg 4140
248 tatattacta taaatcagta tttattaaag ttaagaatat taataatgta ttttaagttt 4200
250 aaaaaaactt ttttgtaaat agtcataatta atataacttt tagcaatata aatattgaat 4260
252 tttcagtact tacgtcatac tgttaatcct cactataatc atcttttttt atcattaata 4320
254 aagagatttt ttggtttttt atgatcatag ctttttagatc 4360
257 <210> SEQ ID NO: 3
258 <211> LENGTH: 372
259 <212> TYPE: DNA
260 <213> ORGANISM: Ehrlichia ruminantium (formerly Cowdria ruminantium)

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262 <220> FEATURE:
263 <221> NAME/KEY: misc_feature
264 <222> LOCATION: (1)..(372)
265 <223> OTHER INFORMATION: Complement to SEQ ID NO:2, nucleotides <1..372
266     Hypothetical dimethyl adenosine transferase
267     Product="lhworfli"
270 <400> SEQUENCE: 3
271 gatccacttt attaaaagta gagttgcaat actataaggt aaatttgcta ttacttttac      60
273 tggtggtttc gctatatattc gtaaataaat atctaataca tctgataata tgaattcata      120
275 ttacattga aattcttttaa taattttatc atgtattggt aataatctac tgtctttctc      180
277 tatagatatt aatttttttag gattcttttt gagtattgaa taagtcattg taccaagtc      240
279 gggaccaatt tcaataaattg aaaaattgct aatgtttcct gcataattaa ctattttatc      300
281 tgtaatatca gttgagtgaa tgaacattg gcttaactct tttttaggat ttatcatgta      360
283 attatcattc at                                     372
286 <210> SEQ ID NO: 4
287 <211> LENGTH: 723
288 <212> TYPE: DNA
289 <213> ORGANISM: Ehrlichia ruminantium (formerly Cowdria ruminantium)
291 <220> FEATURE:
292 <221> NAME/KEY: CDS
293 <222> LOCATION: (1)..(723)
294 <223> OTHER INFORMATION: Corresponds to SEQ ID NO:2, nucleotides 611..1333
295     Hypothetical triosephosphate isomerase
296     Product="lhworf2"
299 <400> SEQUENCE: 4
300 atg tca tta etc atc gtt gct aac tgg aag atg cat ggt gat ttt ttt      48
301 Met Ser Leu Leu Ile Val Ala Asn Trp Lys Met His Gly Asp Phe Phe
302 1          5          10          15
304 act ttt tct tgg ttt aca aag gag ctt agt aac cgt tta att aat ata      96
305 Thr Phe Ser Ser Phe Thr Lys Glu Leu Ser Asn Arg Leu Ile Asn Ile
306          20          25          30
308 gaa gat aaa gta aag gta gta tta tgc cca cca ttt att gcg tta tct      144
309 Glu Asp Lys Val Lys Val Val Leu Cys Pro Pro Phe Ile Ala Leu Ser
310          35          40          45
312 act tat gtt aat tgt cca cat aat att aag ttt ggt gga cag aac tgt      192
313 Thr Tyr Val Asn Cys Pro His Asn Ile Lys Phe Gly Gly Gln Asn Cys
314          50          55          60
316 tgt tat gta tct agt ggg aag tac act gga gaa att agt gct agt atg      240
317 Cys Tyr Val Ser Ser Gly Lys Tyr Thr Gly Glu Ile Ser Ala Ser Met
318 65          70          75          80
320 tta tat aac tct gga tgt agt tat gta ata gtg ggt cac tct gaa agg      288
321 Leu Tyr Asn Ser Gly Cys Ser Tyr Val Ile Val Gly His Ser Glu Arg
322          85          90          95
324 agg agt acg ttt cat gaa act gat cat gat gtt agg tta aaa gct gaa      336
325 Arg Ser Thr Phe His Glu Thr Asp His Asp Val Arg Leu Lys Ala Glu
326          100         105         110
328 tgt gcg atc gaa tca gga tta ata cca att att tgt gtt gga gaa act      384
329 Cys Ala Ile Glu Ser Gly Leu Ile Pro Ile Ile Cys Val Gly Glu Thr
330          115         120         125

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332 tta cta gat agg gaa aat ggt atg cta aaa gat act tta tta agt caa      432
333 Leu Leu Asp Arg Glu Asn Gly Met Leu Lys Asp Thr Leu Leu Ser Gln
334      130      135      140
336 tgt agt gaa tct ttt cct aaa aat ggt aag ttt atc ata gca tat gag      480
337 Cys Ser Glu Ser Phe Pro Lys Asn Gly Lys Phe Ile Ile Ala Tyr Glu
338 145      150      155      160
340 cca gta tgg gca ata ggg aac aat aaa ata cct tct act gat gta ata      528
341 Pro Val Trp Ala Ile Gly Asn Asn Lys Ile Pro Ser Thr Asp Val Ile
342      165      170      175
344 ata gaa gct tta gag att att agg tca tat gat tat gta tct gat atc      576
345 Ile Glu Ala Leu Glu Ile Ile Arg Ser Tyr Asp Tyr Val Ser Asp Ile
346      180      185      190
348 ata tat ggt gga gca gta aat cat act aat gta ggt gat att gta agt      624
349 Ile Tyr Gly Gly Ala Val Asn His Thr Asn Val Gly Asp Ile Val Ser
350      195      200      205
352 atc aat caa ttg tct ggt gtt tta gtt ggt agt gct agt tta gat atg      672
353 Ile Asn Gln Leu Ser Gly Val Leu Val Gly Ser Ala Ser Leu Asp Met
354      210      215      220
356 gag agt ttt ttt aat ata ata tgt agt gct ata aat gtg agg caa agt      720
357 Glu Ser Phe Phe Asn Ile Ile Cys Ser Ala Ile Asn Val Arg Gln Ser
358 225      230      235      240
360 taa      723
363 <210> SEQ ID NO: 5
364 <211> LENGTH: 240
365 <212> TYPE: PRT
366 <213> ORGANISM: Ehrlichia ruminantium (formerly Cowdria ruminantium)
368 <400> SEQUENCE: 5
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371 1      5      10      15
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375      20      25      30
378 Glu Asp Lys Val Lys Val Val Leu Cys Pro Pro Phe Ile Ala Leu Ser
379      35      40      45
382 Thr Tyr Val Asn Cys Pro His Asn Ile Lys Phe Gly Gly Gln Asn Cys
383      50      55      60
386 Cys Tyr Val Ser Ser Gly Lys Tyr Thr Gly Glu Ile Ser Ala Ser Met
387 65      70      75      80
390 Leu Tyr Asn Ser Gly Cys Ser Tyr Val Ile Val Gly His Ser Glu Arg
391      85      90      95
394 Arg Ser Thr Phe His Glu Thr Asp His Asp Val Arg Leu Lys Ala Glu
395      100      105      110
398 Cys Ala Ile Glu Ser Gly Leu Ile Pro Ile Ile Cys Val Gly Glu Thr
399      115      120      125
402 Leu Leu Asp Arg Glu Asn Gly Met Leu Lys Asp Thr Leu Leu Ser Gln
403      130      135      140
406 Cys Ser Glu Ser Phe Pro Lys Asn Gly Lys Phe Ile Ile Ala Tyr Glu
407 145      150      155      160
410 Pro Val Trp Ala Ile Gly Asn Asn Lys Ile Pro Ser Thr Asp Val Ile
411      165      170      175

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VERIFICATION SUMMARY

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Input Set : A:\EP.txt

Output Set: N:\CRF3\03112002\J081051.raw

L:18 M:270 C: Current Application Number differs, Replaced Current Application No

L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:2572 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29

L:2573 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29

L:2614 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30

L:3467 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38

L:3936 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43

L:7013 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81

L:7053 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82

L:7054 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82

L:7092 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83

L:8408 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103